

## REMARKS

Claims 1-40 constitute the pending claims in the present application. Applicants respectfully request reconsideration in view of the following remarks. Issues raised by the Examiner will be addressed below in the order they appear in the prior Office Action.

1-4. Applicants note that the previous amendment was entered and considered, and that claims 1-13 and 23-36 are withdrawn as being directed to a non-elected invention. Applicants will cancel such claims upon indication of allowable subject matter.

5. Applicants note that item BX on the previous IDS was not considered. This item will not be resubmitted.

6. Claims 14-22 and 37-40 are rejected under 35 U.S.C. § 101 because the claimed invention allegedly lacks patentable utility. Applicants respectfully traverse this rejection.

Faye et al., WO 99/07836, cited as reference BV in the IDS filed January 29, 2001, discloses nucleotide and amino acid sequences with strong similarity to SEQ ID Nos. 13 and 14. For example, SEQ ID No. 2 of Faye et al. differs from SEQ ID No. 14 of the present application by merely six amino acids, 98% identity (see sequence comparison attached as Exhibit A). On page 8, lines 30-36, Faye et al. state that cells transformed by a plasmid encoding SEQ ID No. 2 (CaCIV1) rescues *S. cerevisiae* cells which lack a functional ScCIV1 gene, a gene essential for cell viability. Accordingly, an agent which blocks the function of CaCIV1 would be expected to exhibit antifungal activity. Applicants asserted that the claimed subject matter was useful for drug screening assays on page 4, lines 5-6, and page 9, lines 11-18, and Faye et al. demonstrate the accuracy of these assertions.

Moreover, Applicants submit that use as a diagnostic tool, despite the Office Action's assertions to the contrary, is a *specific and substantial* utility that was asserted in the present application. The mere fact that other sequences may also be used for this purpose does not contradict this utility, or make it any less specific. For example, many different compounds have been identified – and patented – as antidepressant pharmaceuticals. The mere fact that *one* antidepressant is known does not make subsequent compounds identified as having similar

activity any less useful, nor their utility any less specific, as the arguments recited in the Office Action suggest. Accordingly, the mere fact that other nucleic acids identified and sequenced from *C. albicans* could be used for diagnostic purposes does not undercut the fact that the presently claimed subject matter could also be used to diagnose the presence of *C. albicans* in a patient. Contrary to the statements in the Office Action, it is not true that *any* nucleic acid would have this utility. This utility is dependent on the particular sequence disclosed by Applicants, and random sequences would typically be ineffective for this purpose. This fact demonstrates that the asserted utility is, in fact, specific.

For the reasons set forth above, Applicants submit that the pending claims fully comply with the requirements of 35 U.S.C. § 101. Reconsideration and withdrawal of this rejection is respectfully requested.

With respect to the rejection of these claims as not being enabled because the claimed invention was not allegedly supported by a utility, Applicants submit that the uses described above were described in the application with sufficient detail and clarity that one of skill in the art could have practiced the claimed invention throughout its scope. Reconsideration and withdrawal of this rejection is respectfully requested.

7. Claims 37-40 are rejected under 35 U.S.C. §112, first paragraph, as allegedly containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention. Applicants respectfully traverse this rejection to the extent it is maintained over the claims as amended.

Applicants have amended claim 37 to more particularly point out conditions recited on page 13 of the application. Reconsideration and withdrawal of this rejection is respectfully requested.

8. Claims 37-40 are rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite. Applicants respectfully traverse this rejection to the extent it is maintained over the claims as amended.

Applicants have amended claim 37 as pointed out above. Applicants submit that hybridization is a common laboratory technique, and that one of skill in the art would readily be able to determine whether or not a nucleic acid sequence hybridizes to another under specified conditions. Reconsideration and withdrawal of this rejection is respectfully requested.

### **CONCLUSION**

In view of the foregoing amendments and remarks, Applicants submit that the pending claims are in condition for allowance. Early and favorable reconsideration is respectfully solicited. The Examiner may address any questions raised by this submission to the undersigned at 617-951-7000. Should an extension of time be required, Applicants hereby petition for same and request that the extension fee and any other fee required for timely consideration of this submission be charged to **Deposit Account No. 18-1945**.

Respectfully Submitted,

Date: July 5, 2001

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JUL 09 2001



# results of BLAST

## BLASTP 2.1.3 [Apr-11-2001]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 992903094-22877-12488

**Query=**

(339 letters)

**Database:** pat

71,783 sequences; 10,525,338 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

### Distribution of 503 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

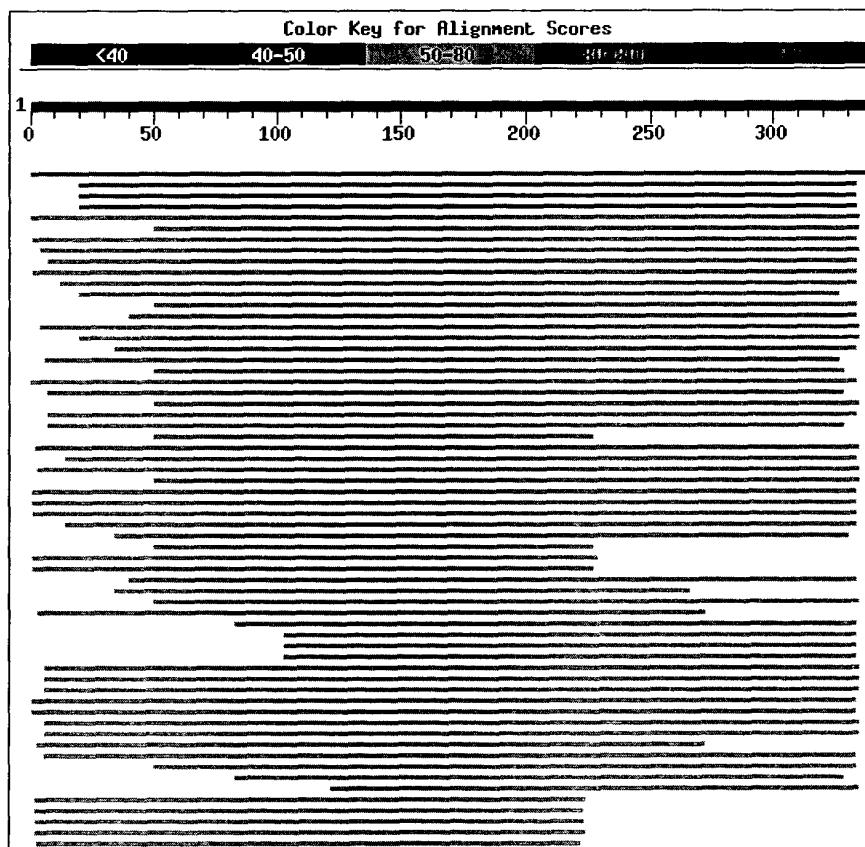


EXHIBIT A

## Sequences producing significant alignments:

				Score (bits)	E Value
gi 9928920	emb CAC05182.1	(AX005954)	unnamed protein produ...	624	e-179
gi 6733419	emb CAB69315.1	(A84499)	unnamed protein product...	82	4e-16
gi 10061049	gb AAE37002.1	Sequence 2 from patent US	5986055	82	4e-16
gi 6733417	emb CAB69314.1	(A84497)	unnamed protein product...	82	4e-16
gi 11340555	emb CAC17042.1	(AX040958)	unnamed protein prod...	78	9e-15
gi 12225900	emb CAC21767.1	(AX048754)	unnamed protein prod...	76	4e-14
gi 11340559	emb CAC17043.1	(AX040962)	unnamed protein prod...	74	8e-14
gi 10057862	gb AAE34768.1	Sequence 5 from patent US	5977442	74	8e-14
gi 2491504	gb AAB79640.1	I64354	Sequence 2 from patent US 5...	74	1e-13
gi 5950570	gb AAE04796.1	Sequence 2 from patent US	5869043	73	2e-13
gi 10057864	gb AAE34770.1	Sequence 7 from patent US	5977442	72	5e-13
gi 10057863	gb AAE34769.1	Sequence 6 from patent US	5977442	71	7e-13
gi 4001196	gb AAC94628.1	AR025720	Sequence 20 from patent U...	71	7e-13
gi 10057861	gb AAE34767.1	Sequence 4 from patent US	5977442	71	1e-12
gi 11340563	emb CAC17044.1	(AX040966)	unnamed protein prod...	70	2e-12
gi 12827408	gb AAE50558.1	Sequence 17 from patent US	6114517	69	3e-12
gi 1831632	gb AAB46086.1	Sequence 16 from patent US	559590...	69	3e-12
gi 4001195	gb AAC94627.1	AR025719	Sequence 19 from patent U...	69	4e-12
gi 12225904	emb CAC21768.1	(AX048758)	unnamed protein prod...	68	6e-12
gi 5955786	gb AAE07442.1	Sequence 9 from patent US	5801015	68	8e-12
gi 10057859	gb AAE34765.1	Sequence 2 from patent US	5977442	68	8e-12
gi 10058203	gb AAE35109.1	Sequence 2 from patent US	5981248	68	9e-12
gi 5955788	gb AAE07444.1	Sequence 11 from patent US	5801015	67	1e-11
gi 12225908	emb CAC21769.1	(AX048762)	unnamed protein prod...	67	1e-11
gi 10057860	gb AAE34766.1	Sequence 3 from patent US	5977442	67	2e-11
gi 1831631	gb AAB46085.1	Sequence 15 from patent US	559590...	66	3e-11
gi 14100016	gb AAE53156.1	Sequence 24 from patent US	6140124	66	4e-11
gi 1831630	gb AAB46084.1	Sequence 14 from patent US	559590...	65	5e-11
gi 10058204	gb AAE35110.1	Sequence 4 from patent US	5981248	65	5e-11
gi 10049308	gb AAE26215.1	Sequence 2 from patent US	5948885	65	6e-11
gi 5942087	gb AAE01619.1	Sequence 3 from patent US	5858765	65	6e-11
gi 3997995	gb AAC91427.1	AR017537	Sequence 14 from patent U...	65	6e-11
gi 6733351	emb CAB69295.1	(A84431)	unnamed protein product...	65	6e-11
gi 6733369	emb CAB69304.1	(A84449)	unnamed protein product...	65	6e-11
gi 10051523	gb AAE28430.1	Sequence 33 from patent US	5958784	65	7e-11
gi 2491506	gb AAB79642.1	I64356	Sequence 4 from patent US 5...	64	9e-11
gi 12225892	emb CAC21765.1	(AX048746)	unnamed protein prod...	64	1e-10
gi 1609068	gb AAB12024.1	Sequence 4 from patent US	5512473...	64	1e-10
gi 10051521	gb AAE28428.1	Sequence 31 from patent US	5958784	64	1e-10
gi 3715669	emb CAA03585.1	(A61243)	CYCLIN-DEPENDENT KINASE...	64	1e-10
gi 6733343	emb CAB69291.1	(A84423)	unnamed protein product...	63	3e-10
gi 6733361	emb CAB69300.1	(A84441)	unnamed protein product...	63	3e-10
gi 1831627	gb AAB46081.1	Sequence 11 from patent US	559590...	63	3e-10
gi 1831622	gb AAB46076.1	Sequence 2 from patent US	5595904...	63	3e-10
gi 14107100	gb AAE55954.1	Sequence 18 from patent US	6165461	63	3e-10
gi 6733349	emb CAB69294.1	(A84429)	unnamed protein product...	63	4e-10
gi 12827407	gb AAE50557.1	Sequence 15 from patent US	6114517	63	4e-10
gi 6733367	emb CAB69303.1	(A84447)	unnamed protein product...	63	4e-10
gi 14100017	gb AAE53157.1	Sequence 46 from patent US	6140124	62	4e-10
gi 2491505	gb AAB79641.1	I64355	Sequence 3 from patent US 5...	62	4e-10
gi 10188272	emb CAC09126.1	(AX027295)	unnamed protein prod...	62	5e-10
gi 10188270	emb CAC09125.1	(AX027293)	unnamed protein prod...	62	5e-10
gi 5976240	gb AAE13650.1	Sequence 4 from patent US	5830699...	61	1e-09
gi 10057865	gb AAE34771.1	Sequence 8 from patent US	5977442	61	1e-09
gi 1252508	gb AAA93767.1	Sequence 2 from patent US	5459036	61	1e-09
gi 10067610	gb AAE40373.1	Sequence 8 from patent US	6001580	61	1e-09
gi 10051520	gb AAE28427.1	Sequence 30 from patent US	5958784	61	1e-09
gi 3012816	gb AAC11659.1	I76662	Sequence 43 from patent US ...	60	2e-09

gi 10051525 gb AAE28432.1	Sequence 35 from patent US 5958784	60	2e-09
gi 14103310 gb AAE54744.1	Sequence 2 from patent US 615341...	59	3e-09
gi 10051519 gb AAE28426.1	Sequence 29 from patent US 5958784	59	3e-09
gi 12813502 gb AAE44802.1	Sequence 31 from patent US 6083713	59	4e-09
gi 1831624 gb AAB46078.1	Sequence 6 from patent US 5595904...	58	7e-09
gi 3997604 gb AAC91034.1	AR017146 Sequence 6 from patent US...	58	8e-09
gi 1831629 gb AAB46083.1	Sequence 13 from patent US 559590...	58	8e-09
gi 12225932 emb CAC21775.1	(AX048786) unnamed protein prod...	58	9e-09
gi 12811293 gb AAE44306.1	Sequence 2 from patent US 6080557	58	1e-08
gi 11340567 emb CAC17045.1	(AX040970) unnamed protein prod...	58	1e-08
gi 9998363 emb CAC07562.1	(AX012313) unnamed protein produ...	57	1e-08
gi 5951591 gb AAE05817.1	Sequence 38 from patent US 586964...	57	2e-08
gi 10057866 gb AAE34772.1	Sequence 9 from patent US 5977442	57	2e-08
gi 10067622 gb AAE40379.1	Sequence 14 from patent US 6001580	56	3e-08
gi 12225888 emb CAC21764.1	(AX048742) unnamed protein prod...	56	3e-08
gi 1831628 gb AAB46082.1	Sequence 12 from patent US 559590...	56	3e-08
gi 6733345 emb CAB69292.1	(A84425) unnamed protein product...	56	3e-08
gi 1831623 gb AAB46077.1	Sequence 4 from patent US 5595904...	56	3e-08
gi 6733363 emb CAB69301.1	(A84443) unnamed protein product...	56	3e-08
gi 11340599 emb CAC17053.1	(AX041002) unnamed protein prod...	56	3e-08
gi 2830527 gb AAC00731.1	I68405 Sequence 2 from patent US 5...	56	4e-08
gi 5985705 gb AAE16513.1	Sequence 14 from patent US 5837853	56	4e-08
gi 5976242 gb AAE13652.1	Sequence 6 from patent US 5830699...	55	6e-08
gi 6779545 emb CAB70484.1	(A95607) unnamed protein product...	55	6e-08
gi 10051515 gb AAE28422.1	Sequence 25 from patent US 5958784	54	1e-07
gi 2489140 gb AAB77276.1	I57261 Sequence 13 from patent US ...	54	1e-07
gi 2830537 gb AAC00741.1	I68415 Sequence 30 from patent US ...	54	1e-07
gi 10052141 gb AAE29048.1	Sequence 6 from patent US 5962232	54	2e-07
gi 12813500 gb AAE44800.1	Sequence 29 from patent US 6083713	54	2e-07
gi 10051526 gb AAE28433.1	Sequence 36 from patent US 5958784	53	2e-07
gi 10051513 gb AAE28420.1	Sequence 23 from patent US 5958784	53	3e-07
gi 2725137 gb AAB92819.1	I67157 Sequence 25 from patent US ...	53	3e-07
gi 5944578 gb AAE02654.1	Sequence 9 from patent US 5861300...	53	3e-07
gi 2489138 gb AAB77274.1	I57259 Sequence 11 from patent US ...	52	3e-07
gi 10043358 emb CAC07738.1	(AX019387) unnamed protein prod...	52	3e-07
gi 5976239 gb AAE13649.1	Sequence 3 from patent US 5830699...	52	4e-07
gi 5942086 gb AAE01618.1	Sequence 2 from patent US 5858765	52	4e-07
gi 6731333 emb CAB69156.1	(A80507) unnamed protein product...	52	4e-07
gi 6001914 gb AAE22876.1	Sequence 2 from patent US 5854392	52	5e-07
gi 12225880 emb CAC21762.1	(AX048734) unnamed protein prod...	52	5e-07
gi 12225896 emb CAC21766.1	(AX048750) unnamed protein prod...	52	5e-07
gi 12225920 emb CAC21772.1	(AX048774) unnamed protein prod...	52	6e-07

### Alignments

>gi|9928920|emb|CAC05182.1| (AX005954) unnamed protein product [Candida albicans]  
Length = 339

Score = 624 bits (1609), Expect = e-179  
Identities = 333/339 (98%), Positives = 335/339 (98%)

Query: 1 MKLSDYYIDKELIYNSAISDIYTAIDKFNNLPVCLKIVDEDFSLPPHSIHREIFILKTLK 60  
MKLSDYYIDKELIYNSAISDIYTAIDKFNNLPVCLKIVDEDFSLPPHSIHRE+ ILKTLK  
Sbjct: 1 MKLSDYYIDKELIYNSAISDIYTAIDKFNNLPVCLKIVDEDFSLPPHSIHREVLILKTLK 60

Query: 61 PHPNIIIEYFNDLK IYDDVILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQYTL 120  
PHPNIIIEYFNDLK I DD+ILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQYTL  
Sbjct: 61 PHPNIIIEYFNDLKICDDIILVTKLYRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQYTL 120

Query: 121 ANEIEEKDIKLWLKSMSGLEFIHSQGIIHRDIKPSNIFFARDITQPIIGDFDICYDLK 180  
ANEIEEKDIKLWLKSMSGLEFIHSQGIIHRDIKPSNIFFARDITQPIIGDFDICYDLK  
Sbjct: 121 ANEIEEKDIKLWLKSMSGLEFIHSQGIIHRDIKPSNIFFARDITQPIIGDFDICYDLK 180

Query: 181 LPPKDEPPMAKYIDVSTGIYKAPELILGITNYEYEIDIWSLGIIILTGLYSENFQSVLVKD 240

PPKDEPPMAKYIDVSTGIYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKD  
 Sbjct: 181 SPPKDEPPMAKYIDVSTGIYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKD 240

 Query: 241 DKELTNDSHVSDLYLLNQIFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYPRKDW 300  
 DKELTNDSHVSDLYLLNQIFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYPRKDW

 Sbjct: 241 DKELTNDSHVSDLYLLNQIFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYPRKDW 300

 Query: 301 DIILPRCNDDLMKEIFTKMIKYDRSKRITSKEILQLMLD 339  
 DIILPRCNDD MKEIFTKMIKYDRSKRITSKEILQLMLD

 Sbjct: 301 DIILPRCNDDFMKEIFTKMIKYDRSKRITSKEILQLMLD 339

>gi|6733419|emb|CAB69315.1| (A84499) unnamed protein product [unidentified]  
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Score = 82.2 bits (202), Expect = 4e-16  
 Identities = 82/316 (25%), Positives = 141/316 (43%), Gaps = 54/316 (17%)

Query: 21 IYTAIDKFNNLPVCLKIV--DEDFLPPIHREIFILKTLKPHPNIEYFNDLKIYDDV 78  
 +Y A +K V LK + D + P + REI +LK L HPNI++ + + + +  
 Sbjct: 264 VYKARNKLTGEVVALKKIRLDTEGVPSTAIREISLLKELN-HPNIVKLLDVIHTENKL 322

 Query: 79 ILVTKLRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQYTLANEIEEKDIKLWLKSMSS 138  
 LV + DL + ++ + + GI L IK +L +  
 Sbjct: 323 YLVFEFLHQDLKKFMDASA-----LTGIPPLPL-----IKSYLFQLLQ 359

 Query: 139 GLEFIHSQGIIHRDIKPSNIFFARDDITQPIIGDFDICYDLKLPKDEPPMAKYIDVSTG 198  
 GL F HS ++HRD+KP N+ + + DF + +P + +V T  
 Sbjct: 360 GLAFCHSHRVLHRDLKPQNLLINTEGAIK--LADFGLARAFGVPVRTYTH----EVVTL 412

 Query: 199 IYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKDDKELTNDHVSDLYLLNQ 258  
 Y+APE++LG Y +DIWSLG I + +V DS + L+ +  
 Sbjct: 413 WYRAPEILLGSKYYSTAVDIWSLCIF-----AEMVTRRALFPGDSEIDQLF---R 460

Query: 259 IFENFGTPNLTDFEDELFCDEYNNENLHFKKFNLQKYPRKDWDIILPRCNDDLMKEIFTK 318  
 IF GTP+ + +Y K + K+ R+D+ ++P ++D + + ++  
 Sbjct: 461 IFRTLGTDPDEVVWPGBTMSPDY-----KPSFPKWARQDFSKVVPPLDED-GRSLLSQ 511

Query: 319 MIRYDRSKRITSKEIL 334  
 M+ YD +KRI++K L  
 Sbjct: 512 MLHYDPNKRISAKAAL 527

>gi|10061049|gb|AAE37002.1| Sequence 2 from patent US 5986055  
 Length = 298

Score = 82.2 bits (202), Expect = 4e-16  
 Identities = 82/316 (25%), Positives = 141/316 (43%), Gaps = 54/316 (17%)

Query: 21 IYTAIDKFNNLPVCLKIV--DEDFLPPIHREIFILKTLKPHPNIEYFNDLKIYDDV 78  
 +Y A +K V LK + D + P + REI +LK L HPNI++ + + + +  
 Sbjct: 18 VYKARNKLTGEVVALKKIRLDTEGVPSTAIREISLLKELN-HPNIVKLLDVIHTENKL 76

 Query: 79 ILVTKLRYDLSQLIEITKYCKRTTRFIYGINGNLVSNQYTLANEIEEKDIKLWLKSMSS 138  
 LV + DL + ++ + + GI L IK +L +  
 Sbjct: 77 YLVFEFLHQDLKKFMDASA-----LTGIPPLPL-----IKSYLFQLLQ 113

 Query: 139 GLEFIHSQGIIHRDIKPSNIFFARDDITQPIIGDFDICYDLKLPKDEPPMAKYIDVSTG 198  
 GL F HS ++HRD+KP N+ + + DF + +P + +V T  
 Sbjct: 114 GLAFCHSHRVLHRDLKPQNLLINTEGAIK--LADFGLARAFGVPVRTYTH----EVVTL 166

 Query: 199 IYKAPELILGITNYEYEIDIWSLGIILTGLYSENFQSVLVKDDKELTNDHVSDLYLLNQ 258